

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2001, 10:01:49 ; Search time 2052.79 Seconds
(without alignments)
12935.110 Million cell updates/sec

Title: US-09-587-111-4
Perfect score: 2809
Sequence: 1 ggctagcctgctctgacagg.....aaaaaaaaaaaaaaaaaa 2809

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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BASE COUNT 497 a 630 c 612 g 531 t
ORIGIN
Query Match 53.6%; Score 1505.8; DB 192; Length 2270;
Best Local Similarity 81.1%; Pred. No. 0;
Matches 1822; Conservative 0; Mismatches 397; Indels 28; Gaps 5;
QY 487 ttcacagcgcagcagcgaatcgcgcctcagataagagtcacactcaactcgaag 546
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DB 12 TTCACAGGAGAGACGGAACTTCCTCCCTCAAGTTAAGTGAATCTCAACGCAAG 71
QY 547 ggaacagctgcagtcagtcagcgcgaatccaaacgaattgcagagatcgctctcaatgcg 606
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QY 607 gctcccgagggttcgcgcgaagatcgcgtgcagctccagatcgaatcgaagcgaagc 666
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DB 132 GCTCCCGGGGTCTCCCGAGAGCTGACTGACTGCTATGAGTACCTGGCGCGACAGC 191
QY 667 aagtaactacagcagcgaatacacagagagcgtccacagagtaagagcgtgcagtaag 726
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QY 727 gctgtcgtcaacctaagaagcaggaatgcagtcagctcagctcagctcagctcagctcag 786
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QY 787 aaggaactcgcgaatcctcaagccctgcgtgaatgcagctgcagctgcagctgcagctgc 846
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QY 847 ggcacagcgcctcgcacatcgccatcgaagaagagagctgcagctgcgtgcagctgcgtg 906
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QY 2164 aaattcaacatcgtgcatggagctgcctcctcagggagcagctgcactccgggcatg 2223
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DB 1686 AAGTTCAACCATTTGATGATGGTGTAGCTGCTTCCAGGAACACTGCGCTTGTGCGGGTG 1745
QY 2224 gtgcgtc 2283
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DB 1746 GTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1805

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Oy	2344	ctgcgaagaagcaltctcgtctccttgagatggaagaatggctctatgtgtgtcagaagaag-	2402
Db	1866	ttgcgaagaagccatctctgtcttgagagatgagaatggttactgtgtgtgacgagaaa	1925
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Oy	2461	cgctgtgcttcacaggttggaagaggttgaacgtggagcttcacatggagcagaagcgtgcagag	2520
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VERSION	AU141855.1	GI:1100376	
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 793)		
	Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,		
	Yanamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and		
	Isogai,T.		
TITLE	HRI human cDNA project		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Takao Isogai		
	Genomics Laboratory		
	Helix Research Institute		
	1532-3 Yana, Kisarazu, Chiba 292-0812, Japan		
	Tel: 81-438-52-3951		
	Fax: 81-438-52-3952		
	Email: genomics@hri.co.jp		
	HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix		
	Research Institute; cDNA library construction; Department of		
	Virology, Institute of Medical Science, University of Tokyo, and		
	Helix Research Institute.		
FEATURES	Location/Qualifiers		
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BASE COUNT	184 a 229 c 230 g 147 t 3 others		
ORIGIN			

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Best Local	Similarity	98.5%	Pred. No. 3.5e-161		
Matches	782	Conservative	0	Mismatches	10
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				Gaps	2
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QY	263	aggccaacacgagcgcgagcttgaggagaaagacaggaaccttgaatctccatctgcaca	322		
Db	61	AGGCCAACACCCACGAGCGGCGCTGGGGGAAAGACAGACCCCTTGACATCTCCACACA	120		
QY	323	ggagctccctgctcgagaccgagagccctccctccctccctcctcctcctcctcctcctc	382		
Db	121	GAGGTCCTGCTGGACCGAGCCAGCTCTCTCTCTTAGATGACCTCACCTTCAGCTTTC	180		
QY	383	caatttcagcttgtagaacatcatagatctgagagcacaagaatctgctctcagcgagag	442		
Db	181	CAGTTTTCAGTTGGAGACATTAGATGGAGGCGCAAGAAAGATGGCTTGAGCGCGAGACAG	240		
QY	443	gaaagctggaattttgggagcgagcttgctcccatggagtcaaatctcagggcgagagac	502		
Db	241	GAAACCTGATTTTGGGACCGGGCTCCCTCCATGGAGTCAACAGTTCAGGCGAGGACC	300		
QY	503	ggaatttcgccccctcaagataagagatcaactcaactcaacgcaagaaaggaaagttgcaagtc	562		
Db	301	GGAAATTCCTCCCTCAGATTAAGAGTCAACTCACTACGGAAGGAAAGACAGTGCACAGTC	360		
QY	563	agccgagatccaaacggaatttgaacgagatcggtcttcaatctgagcttcgaggtgctcc	622		
Db	361	AGCCGAGATCCAAACCGATTTGACCGAGATCGGCTTTCATATGGGGCTCCCGGGGTTCC	420		
QY	623	ccgagagatctggtctggaacttccaagtagtaacctgaagacccagcaagtaacctcaacgact	682		
Db	421	CCGAGAGATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACAGCAAGTACCTCACCGACT	480		
QY	683	cggaatacacagagagctcacagagtaagagctgaccttgaaggagctgtgcgtgaactta	742		
Db	481	CGGATACACAGAGGGCTCCACAGGTAACAGCTGCTGATGAAGGCTGTGCTGAACCTTA	540		
QY	743	aggacggaatcaatgctctgcatctctgcacactgtctgcagatcgacagagactctggcaatc	802		
Db	541	AGGACGGAGTCAATGGCTGCTCATTTCCACTGTGTCAGATTCACAGAGGACTGCGCAATC	600		
QY	803	ctccagccccctggttaaatgcccagctgcacagatagactattaccgagggccacagcgtctgc	862		
Db	601	CTCCAGCCCCCTGGTAAATGCCAGTCGACAGATGACTATTACCGAGGCCACACGCTCTCC	660		
QY	863	acaatcgcaatagaagaagagatctgcaatgtgtgaagctcctgtgtgagaaatgagagca	922		
Db	661	ACATGCGCAATTAGAAAGAGAGAGTCTGCATATGTGTGAAGCTTCTGTTGGAGAAATGGGGCA	720		
QY	923	atgtcatagccccgagctcgagccgctcttccagaaggccaagggacttgcatttalt	982		
Db	721	ATGTGATATCCC -GGCTTCGGGCGG -TTTTCACAGAAAGCAAGGAGACTTCTTTAAT	778		
QY	983	tcggtgagctacc 996			
Db	779	TCGGGAGCTTACC 792			
RESULT	3				
LOCUS	BG254423	953 bp	mRNA	EST	13-FEB-2001
DEFINITION	603269021P1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:447157 5',				
ACCESSION	BG254423				
VERSION	BG254423.1	GI:12762439			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

REFERENCE 1 (bases 1 to 953)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DRP
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 DNA distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM10305 row: j column: 06
 High quality sequence stop: 676.

FEATURES
 source 1..953
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 /db_xref="taxon:9606"
 /clone="IMAGE:447157"
 /clone_11b="NIH_MGC_91"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 201 a 284 c 269 g 199 t
 ORIGIN

Query Match 23.2%; Score 651.4; DB 175; Length 953;
 Best Local Similarity 95.8%; Pred. No. 1.9e-137;
 Matches 702; Conservative 0; Mismatches 26; Indels 5; Gaps 3;

QY 852 cagcgctcgcacatcgacatgagaagagagctgca-gtgtgaaagctcctgtg 910
 DB 1 CAGCGCTCGCAGCATCGCATGAGAGAGAGAGTGTGTAAGCTCTGTGTG 60
 QY 911 aaaaatggggcgaatgctgctgcccggcgctgcccgtcttcccaaggcgaagg 970
 DB 61 AGAATGGGGCCAAATGCTGATGCCGGGCGCGCGCTTCTCCAGAGGCCAAGG 120
 QY 971 ctgtcttattatcgtgagctacccctcctctgtgcccgttcgacaaagcagtg 1030
 DB 121 CTTGCTTTATTTCCGTGAGCTACCCCTCTCTTGGCGCGCTTGACCAAGCA 180
 QY 1031 tggtaagctactcctcgtggaacacacacgcgcagcctgcaagccactgact 1090
 DB 181 TGGTAAGCTACCTCCCTGGAGAACCCACACAGCCCGCAGCTGACACTGACT 240
 QY 1091 aagggaacacacatcctcgtgctgctgtagtatactcggacaactagctggaac 1150
 DB 241 AGGGCAACAGAGCTCGATGCCCTAGTAGTATGCGACAACCTCAGCTGAAG 300
 QY 1151 caactggtgacacagatgatagtggtcctcgaacgtgggcccgcctcgtccac 1210
 DB 301 CACTGCTGACAGCATGTATGATGGGCTCTCCAACTGGGGCGCGCTCTGCT 360
 QY 1211 tgcagctgagagacatcgcaacctgcaagatctcagcctctgaagctggcc 1270
 DB 361 TGCAGCTTGAAGACATCCCAACTGACAGATCTCAGCCTCTGAAGCTGGCG 420
 QY 1271 aagggaagctcgaagcttctcgaagcaactcgtgagggagagcttctgaag 1330
 DB 421 AGGGCAAGATTCAGATTTTCAGGCAATCTCTCAGCGGAGATTTTCAGGCA 480
 QY 1331 ttccccaagctcagcagagtggtgctatcggcctgtccgggtgtcgtcgtatg 1390
 DB 481 TTTCCGAAGATTCAACGAGTGTGTATGGGCTGTCCGGGTGTGCTGTATGAC 540

QY 1391 ctctctgagcagctgttgaggaaactcagctgtgagatcattccttcattgca 1450
 DB 541 CTTCTGTGAGCCGCTGTGAGAGAACTCATGCTGTGAGATCATTTGCTTCA 600
 QY 1451 gccccagccagcagcgaatggtcgttttgagccctgacaacatcgtcgcagg 1510
 DB 601 GCCCGACGACGACCAAGATGTCG-TTTGGAGCCCGAACAACATGTCAC 659
 QY 1511 gggatcgtcaccacacagctctcttcttctcgtgtgatactgacatcat 1570
 DB 660 TGGGATCTGTGATTCACCAAGTTCTTTAACCCTGTGT-ATCGATCTAC 716
 QY 1571 tcttcacgcgtg 1583
 DB 717 CTTTCACCGCTGT 729

RESULT 4
 BE689928 840 bp mRNA EST 22-DEC-2000
 LOCUS 602186482P1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298445 5',
 DEFINITION mRNA sequence.
 ACCESSION BE689928 GI:11975336
 VERSION BE689928.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 840)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DRP
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM1154 row: c column: 22
 High quality sequence stop: 662.

FEATURES
 source 1..840
 Location/Qualifiers
 1..840
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4298445"
 /clone_11b="NIH_MGC_49"
 /tissue_type="melanotic melanoma, high MDR (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; XhoI sites using the following 5' adaptor: GGCAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 174 a 256 c 258 g 152 t
 ORIGIN

Query Match 23.1%; Score 647.8; DB 168; Length 840;
 Best Local Similarity 96.4%; Pred. No. 1.2e-136;
 Matches 716; Conservative 0; Mismatches 22; Indels 5; Gaps 5;

QY 21 ggaagatlaagctccggttcacacgctgcgcgctgagctggagtgaggtgac 80
 DB 1 GGAGATTAGCTCCCGTTCTCACCGTCCGGCTGGCAGGTGGGCTGAGGAT 60

QY 81 gagaccagaacctgtctgtgagcttagtgcctcagagctgggagaggttccgcgc 140
 Db 61 GAGACCAGAACCTGCTTCTGAGCTTAGTGTCTGAGACTGGGAGGGAGTTCGGCCGC 120
 QY 141 tccctgtgtcagagccgagccctcccggtctcactctcctccgagccctgcta 200
 Db 121 TCCCTGTGTGTCAGAGCCGAGCCCTCCGGCTTCACTTCTCCCGACGCCCTGTGCTA 180
 QY 201 ctgagaagctccggagatccagcagcagccgctgtgctcagcctggggggttcag 260
 Db 181 CTGAGAACCTCCGGGATCCAGACGCCCTCCGCTGCTCACTGCGGGCTCCAG 240
 QY 261 tcagagccacacccagcgcagcttgggagagagagacccttgcacatctcacttgc 320
 Db 241 TCAGGCCAACCCGAGCCGAGCTGGAGAGAGAACAGACCTTGCATCTGCATCTGCA 300
 QY 321 cagaggtctcgtctgagcagcagcctcctcctcctagtatgacatccctcagctc 380
 Db 301 CAGAGTCTCTGCTGAGCCGAGCAGCCCTCTCTCTGAGATGACCTCAGCTCCAGCTC 360
 QY 381 tccagtttcaggttggagacattagatggagggcccaagaatggtctctgagcagcag 440
 Db 361 TCCAGTTTTCAGGTTGGAGACATTGATGAGAGCCCAAGAGTGGCTTGAAGCCGAGACG 420
 QY 441 aggaagctgtgatttggagcggcgtgctccctccatggagttcagagtcagagcag 500
 Db 421 AGGAAGCTGGA-TTTGGAGCGGGCTGCTCCCTGAGTACAGTTCGA-CGCGAGGA 478
 QY 501 ccggaatctgccccctcagataagagttcaactcaactacagaaaggagaaaggtgcag 560
 Db 479 CCGGAATTCGCCCTCCAGATGAGAGTCAA-CTCAACTACGGAAGGAGAACGGGCGCAG 537
 QY 561 tcagccagatcc-aaaccgatttgcacagatcgtctcctcctcaatcggtctccggggtg 619
 Db 538 TCAGCGGATTCCAAAACCGATTGACCCAGATCGGCTCTTCAATCGGTCTCCGGGGTG 597
 QY 620 tcccgagagatctggtgagcttccagagatccttgaagcagcagcaagtaactccacg 679
 Db 598 TCCCGAGAGACTGGCTGAGATTCAGAGTACTGAGCGAGCAGCAAGTACTCA-CG 656
 QY 680 actgggaatacagagagaggtcccaaggtlaagagtgctcctatgaagctgtgtcgaac 739
 Db 657 ACTGGGAATACACAGAGGGCCGACAGGATGAGACTGCTGATGAAGCTGTGTGACT 716
 QY 740 ttaagcagcagtcacatgcctgc 762
 Db 717 TAAGAGAGGTCATGCTCTGCTTC 739
 RESULT 5
 AM976725/c 686 bp mRNA EST 02-JUN-2000
 LOCUS EST388834 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
 DEFINITION AM976725
 ACCESSION AM976725
 VERSION AM976725.1 GI:8167958
 KEYWORDS EST.
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS
 Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
 I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
 Quackenbush,J.
 TITLE
 Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element cDNA microarray
 JOURNAL
 COMMENT
 Contact: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@tigr.org

FEATURES
 SOURCE
 Plate: 364
 Seq primer: Forward.
 Location/Qualifiers
 1..686
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="MAGE resequences, MAGE"
 /note="Vector: pBluescriptsm"
 BASE COUNT 124 a 195 c 199 g 168 t
 ORIGIN
 Query Match 22.4%; Score 629.8; DB 123; Length 686;
 Best Local Similarity 96.6%; Pred. No. 1.5e-132;
 Matches 654; Conservative 0; Mismatches 22; Indels 1; Gaps 1;
 QY 272 ccgacgcgagctgggaggaagacagacccttgacatctccatctgacagagttctg 331
 Db 682 CCACGCCAAGCTGGAGAGGAGAAACAGGACCTT-AAATCTCCATCGGCAAGGCTCTG 624
 QY 332 gctgagccgagcagctctcctcctctagatgagctcaaccctcagctctcagtttca 391
 Db 633 GCTGSCCAACCAACTCTCTCTCTAGATGACTCACCTCCAGCTCTCCAGTTTCCA 564
 QY 392 gcttgagacattagatggagcgaagaagatgctcttggagcggagacagagaaagctg 451
 Db 563 GGTGAGACATTAGATGAGAGCCAAAGAAAGATGCTGTGAGCGGAGACAGAGAAAGCTGG 504
 QY 452 atttggagcggcgtgctcctccatggagttcagatctccagggcgaggaatctcg 511
 Db 503 ATTTTGGAGCGGGCTGCTCCCATGAGATCAACATTCAGGCGAGGACCGGAATTCG 444
 QY 512 cccctcagataagatcaactcaactcagaaaggagagtgccagttcagcggatc 571
 Db 443 CCCCTCAATTAAGATCAACTCAACTACCGAAGGAGAACAGTCCAGTCCAGCTGATC 384
 QY 572 caaacggaattgacccgagatcgctctcctcaatgcygcttccggggtgtccccgagatc 631
 Db 383 CAAACCGATTGACCGAGATGCGCTCTTCATGCGGTCTCCGGGGGTGCCCGAGATC 324
 QY 632 tggctgagcttccagagttacttgagcagaagcagcaagtaactcagcagctcgaaata 691
 Db 333 TGGCTGGACTTCCACAGATCACTGAGCAGCAAGACCAAGTACTCTCACCACTCGGAATCA 264
 QY 692 cagaggtctcagcagtagagctgctgagatgaagcgtgtgtgagaccttgaagcaggag 751
 Db 263 CAGAGGCTCCACAGATTAAGAGCTGCTGATGAAGGCTGTGTAACCTTAAGAGCGAGG 204
 QY 752 tcaatgctgcatctgccaactctgacagatcagacagaggaactctgcaactcagcccc 811
 Db 203 TCAATGCTCTGATCTGCGCACTGCTGCAAGTGCAGAGGACTGTGCAATCCTCAGCCCC 144
 QY 812 tggtaaatgcccagtgacagatgactatccaggggcccaagcgctctgcaacatcgcca 871
 Db 143 TGGTAATGCCAGTGCACAGATGACTATTACCGAGGCGCACGCTCTGCACATCGCA 84
 QY 872 ttgaaagagagctgtgagtggtgagagctcctgtgagaaatggggccaatgtgtcatg 931
 Db 83 TTGAAAGAGAGTGTGCAGTGTGTGAAGCTCTGTGTGAAGATGGGCAATGTGCATG 24
 QY 932 cccgggctcgggccgc 948
 Db 23 CCCGGGCTCGGGCCGC 7
 RESULT 6
 AUI36431 841 bp mRNA EST 24-OCT-2000
 LOCUS AUI36431 PLACE1 Homo sapiens cDNA clone PLACE104258 5', mRNA
 DEFINITION AUI36431
 ACCESSION AUI36431
 VERSION AUI36431.1 GI:10996970
 KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 841)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
FEATURES
source
1. 841
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1004258"
/clone.lib="PLACE1"
/tissue.type="Placenta"
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BASE COUNT 193 a 251 c 233 g 151 t 13 others
ORIGIN

Query Match 22.0%; Score 618.4; DB 108; Length 841;
Best Local Similarity 97.9%; Pred. No. 6e-130;
Matches 644; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 32 ctcacgttcacacgctgcgcgctgacaggttgagtgacagagacagagac 91
|||||
Db 1 CTCGCCGTCACACGTCGCCGCTGCGCAGAGTGGCTGAGCGTGCAGACGACGACGAC 60
|||||

QY 92 ctgctgtcgtgagactagtgctcagagctgggagagagaggttcgcgcgtctctgt 151
|||||
Db 61 CTGCTGTGCTGGAGCTTAGTCTCAGAGCTGGGAGGAGGAGTTCGCCGCTCTCTGT 120
|||||

QY 152 cagcgccgagcgcctccgcgctcacttcctcccgacgcccctctactagaagctc 211
|||||
Db 121 CAGCGCCGCGACGCCCTCCCGGCTTCTCTCCCGACGCCCTGCTACTGAGAGCTC 180
|||||

QY 212 cggagtcacagcagcgcgcagcctgctcagcctgcgggctccagtcagagccaaca 271
|||||
Db 181 CGGAGTCCAGCAGCGCCGACGCGCTGCGCTCAGCTGCGGGGCTCCAGTACGACGACCA 240
|||||

QY 272 ccgagcgcagcctgggagagagagagacaccttgacatctcactgcacagaggtccg 331
|||||
Db 241 CCGACCGCAGCTGGGAGGAGGAGGCGCCCTTGACATCTCCATCTGCACAGAGGTCCTG 300
|||||

QY 332 gctgagccagcagcctcctcctcagagtagacccctcagctccagctccagtttca 391
|||||
Db 301 GCTGAGACGACGAGCTCTCTCTCTAGATGATGACTCACCCTCAGCTCTCCAGTTTCA 360
|||||

QY 392 ggttgagacattagatggagagcacaagatggctctgagcgagacagagaaactgg 451
|||||
Db 361 GGTGAGAGCAATTAGATGGAGGCGCAAGAGATGCTCTGAGCGGAGCAGAGGAAAGCTGG 420
|||||

QY 452 attttggagcgagctgctcctccatgatgagtcacagttcc-aggcgagagacggaaattc 510
|||||
Db 421 ATTTTGGAGCGGGGCTGCTCCCTCATGGAGTTCAGTTCCAAAGGACGAGGAAATTC 480
|||||

QY 511 gcccccaataagatcaacctcaactccagaaagagagagagtgccagtcagccggat 570
|||||
Db 481 GCCCCTCAATAAGATCAACCTCACTACCGAAGGAGGAAAGGAGTCCGACTCAACCGGAT 540
|||||

QY 571 ccaaccgattgaccgagatcgctcttcaatgc-gtctccgggggtgtgcccgagga 629
|||||
Db 541 CCAACCGATTGACCGAGATGCTGCTTCAATGCGGGGTCTCCCGGGGTCTCCCGCANGA 600
|||||

QY 630 tctgctgagcttcacagagactgagcagagacagacagagtaacttaactcagctcgaa 687
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Db 601 TMTGCTGGACCTTCAGAGTACTGAGCAAGACCAACAGTACTCTCCAGCTCGGGA 658
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RESULT 7
AI801897/c 616 bp mRNA EST 16-DEC-1999
LOCUS tx28h02.x1 NCI-CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270931 3'
DEFINITION similar to TR:035433 035433 VANILLOID RECEPTOR SUBTYPE 1. ; mRNA
sequence.
ACCESSION AI801897
VERSION AI801897.1 GI:5367369
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 616)
NCI-CGAP htcp://www.ncbi.nlm.nih.gov/nclogap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cge@bcr-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ULNL at: www.bio.lnlnl.gov/bdrp/image/image.html
Insert length: 663 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 456.
FEATURES
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1. 616
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2270931"
/clone.lib="NCI-CGAP_Lu24"
/tissue.type="carcinoid"
/lab.host="DH10B"
/note="Organ: Lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI-CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonalido."
BASE COUNT 129 a 189 c 169 g 128 t 1 others
ORIGIN

Query Match 21.7%; Score 610.2; DB 102; Length 616;
Best Local Similarity 99.4%; Pred. No. 4.1e-128;
Matches 612; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2152 ttggagcttcaaatcaacatcgagatggcgagctgctccagagagagctggac 2211
|||||
Db 616 TTGGAGCTCTTCAAAATTCACATCGGCATGGCGAGACTGCTTCAGAGAGAGCTGCAC 557
|||||

QY 2212 ttccgagcatgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 2271
|||||
Db 556 TTCGCGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 497
|||||

FEATURES	source
Db	2272 cccaacatgcatcatgacctcaatgagcagagaccgtcaacaatgctgccaactgagacgctg 2331
Db	436 CTCACATGCTCATGCTGCCCTCATGAGCCGAGACCGTCAACAGGTGCGCACATGACAGCTGG 437
Oy	2332 agcaltctgaaagctgcaagaaagccatctctgtccctgagatgagaaatgagctattgtg 2391
Db	436 AGCATTCGTAAGACCTGCAGAAAGCCATCTCTGCTTCCGTGAGATGGAATAGCGTATTGGTGG 377
Oy	2392 tgcagaagaagacagacgaggcaggtgtgatgtctgacccgttgacactaaagccagatggcagc 2451
Db	376 TGCAGAGAAACACACGGGCGCAGGTGTGATGCTGACCGCTTGGCAGCTAAGCCAGATGGCCGC 317
Oy	2452 ccgagatgagcgcgtgtgtcttcagaggctgagagagtgagactgggcttcattgagagcagcg 2511
Db	316 CCGGATGAGACCGCTGCTGCTTCAGGGTGCAGAGAGGTGAACCTGGCTTCATGGAGCAGACG 257
Oy	2512 ctgctacgcgtgtgtgagagaccgcgtcaagggcaggtgtctccctcgaaactcgagaacct 2571
Db	256 CTGCGCTACGCTGTGTGAGAGACCCGTCAGGGGCGAGGTGCTCCGAACTCTGAGAACCTT 197
Oy	2572 gtccctggtctccctccccaagagagatgagatgtgtgtctctgagaaaacatgtgtccc 2631
Db	196 GTCCGCGCTCTCCCTCCCAAGAGGATGATGAGGTGTGCTCTGAGAGAAACATATGTGCC 137
Oy	2632 gtccacgctccctcaatgccaaactgagccagatgcagcaagagcgccagagacagagca 2691
Db	136 GTCACAGCTCTCTCAATCCACATGATGCGCCCAATGCACAGAGAGGCCAGAGACAGACGA 77
Oy	2692 gaagatcttcccaacacacatctgtctgtctgtgggtgcccgatgaattctgctgtgcaatla 2751
Db	76 GAGGATCTCTTCCACACACATCTGTGCGCTCTGCGCTCCACAGGAATTCGTGGCGCAATA 17
Oy	2752 tatatttcactaact 2767
Db	16 TATATTATCACTAACT 1
RESULT	8
LOCUS	BF732920 682 bp mRNA EST 30-MAR-2001
DEFINITION	ncal17D01.x1 NCI-CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3435576 3'
ACCESSION	BF732920
VERSION	BF732920.1 GI:12057995
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 682)
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
	Unpublished (1997)
	Contact: Robert Strausberg, Ph.D.
	Email: cgapbs@email.nih.gov
	Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michel
	R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento
	Soares, Ph.D. CDNA Library Arrayed by: Christa Prange, The
	I.M.A.G.E. Consortium DNA Sequencing by: Washington University
	Genome Sequencing Center
	Clone distribution: NCI-CGAP cDNA distribution information can be
	found through the I.M.A.G.E. Consortium/MLNL, send email to:
	info@image.lnl.gov
	Seq primer: -40UP from Gibco
	High quality sequence stop: 412.
	Location/Qualifiers
	1..682

LOCUS	BP940288/c	588 bp	mRNA	EST	22-JAN-2001
DEFINITION	7043f06.x1 NCI-GCAP.k1d11 Homo sapiens cDNA clone IMAGE:3577090 3'				
similar to TR:Q9Y551 Q9Y551 VANILLOID RECEPTOR-LIKE PROTEIN 1. ;					

BASE COUNT 142 a 208 c 181 g 150 t 1 others

ORIGIN

Query Match 21.2%; Score 596.2; DB 168; Length 682;
 Best Local Similarity 94.0%; Pred. No. 6,3e-125;
 Matches 641; Conservative 0; Mismatches 39; Indels 2; Gaps 2;

Y 991 ctaccctctctcttggccgctgtgacccaagcagtgagagtgtgtaagctactctctgag 1050

Db 2 CTAAAGCCCGCTGCGCGCGCGGCAAGCACTGGATGTGTGAAGCTTACTCTCTCGAG 61

Y 1051 aaccacacccagcccgccagcctgtgaagccactgaactctcccaagggaacaagctctgat 1110

Db 62 AACCCACACACACCCACACAGCCTGGAGGCCATGACTCCATGGAACACACCCCTGGAT 121

Y 1111 gccctgagatgatatctggacaacacccagctagaacatctgcaactgtgtgacacagatgat 1170

Db 122 GCCCTAGATGATGATTCGGACACACTGAGAACATTTGCACTGTGTATACCAAGCATGAT 181

Y 1171 gatggctctctccaaagcttggggccgacctctgacctacagctgacgttgaagacatccgc 1230

Db 182 GATGGCTCTCTCCAAAGCTGGGGCCCGCTGTGCCCTTACCGTGAAGCTTGAAGACATCCGC 241

Y 1231 aacctgcagatctcaagcctctgaagcttgccgcgaaggagggcagaatcagagatttc 1290

Db 242 AACCTGCAGGATCTCACCCCTCTGAAGCTGGCCGCAAGGAGGCGCATGAGATTTTTC 301

Y 1291 aggcacatctccagcagcggaagatttcagagactgaagcacccttcccgaaagttcaccgag 1350

Db 302 AGGCACATCTCTGACGCGGAGATTTCACAGACTGAGCCACCTTTCCGAAAGTTACCGCAG 361

Y 1351 tgggtctatgggacctctgcgggtgtgcgtgtgatgaacctgacctctgttggacagctgtgag 1410

Db 362 TGGTCTATGGGCGCTGTCCGGGTGTGGTATGACGTGGGTCTGTGTGGACAGCTGTGAG 421

Y 1411 gagaactaagtgtgagagataatgtgaccttcaatgtgcaagaagcccgacacagcaaatg 1470

Db 422 GAGAACTAGTGTGGAGATATATTCCTTTCAATTCGAAGAGCGCGCACCGACCGAATG 481

Y 1471 gtccgttttggggccccctgaaacaaactgtgtcgaaggaatggagatctgtcatccccaag 1530

Db 482 GTCCGTTTGGAGCCCCCTTAACAAACTGTGTGCAGNCGGAATGGAGATCTGTATCTCTCAG 541

Y 1531 tctctctaactctcctgtgtaactgtgatacatgtatcatcttcaacacgcgtgtgacctac 1590

Db 542 GTTCTCTTGAACCTTCTGTATATGTATGATCTCAATGTTCACTTTCACCGGTGGTGGCTAC 601

Y 1591 catcagctacacctgaagaagc-aggccgccccctcaactcgtgaagcggaaggttgaaaatc 1649

Db 602 CATCAGCTTACTCTTGAAGAGCAAGGTGCTCTTCACCTGGAAGCGGAGGATT- GCAACTT 660

Y 1650 catgctgtgtgacgggacacatc 1671

Db 661 CATGCTGTGTGACCGGTGTCATC 682

/*file-type="fibrothema"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: ovary; Vector: p773D-Pac (Pharmacia) with a
 modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer (5'
 TGTACCACTCTGAAAGTGGAGGCGCGCGGCAATTTTTTTTTTTTTT 3');
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not
 I and Eco RI sites of the modified p773 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo. "

mRNA sequence.
 ACCESSION BF940288
 VERSION BF940288.1 GI:12357608
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 588)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
 Seq. primer: -400P from Gibco
 High quality sequence stop: 492.
 Location/Qualifiers
 1..588
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3577090"
 /clone_1ib="NCI-CGAP_Kid11"
 /lab_host="DH10B"
 /note="Organ: Kidney; Vector: pT7/T3D-Pac (Pharmacia) with a modified polylinker. Site 1: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 110 a 173 c 163 g 142 t
 ORIGIN

Query Match 20.9%; Score 588; DB 171; Length 588;
 Best Local Similarity 100.0%; Pred. No. 4.4e-123; Indels 0; Gaps 0;
 Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

361 atgacctcacccctcagctctcagcttcaagctgagacatagatgagccaaga 420
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 Db 588 ATGACCTCACCCCTCAGCTCTCCAGTTTCAGTTTGAGACATTAGTGGCCAAAGA 529
 |||||||
 QY 421 gatgctctgaagcgagacagagaagctggaatttgggagcgagctgctccatgag 480
 |||||||
 Db 528 GATGCTCTGAGCGGACAGAGAGAAAGCTGATTTGGGAGCGGCTGCCCTCCATGAG 469
 |||||||
 QY 481 tccagcttcaggggaggaagcgaatcgcgccctcagataagatcaaccctcaactc 540
 |||||||
 Db 468 TCACACTTCCAGGGCGAGGACCGAAATTCGCCCTCAGATTAAGATCAACCTCAACTAC 409
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 QY 541 cgaagaaggacagctgacagctcagccgagatccaacagatlttaaccgagatcgagcttc 600
 |||||||
 Db 408 CGAAAGGGAACAGCTCCAGTCCAGCGGATCCAAACGATTTAGCCAGATGCGCTTTC 349
 |||||||
 QY 601 aatgcggtcccgagggtgtcccgagagatctggtctggaattccagagtaactgagcaag 660
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 Db 348 AATGCGGTCTCCCGGGGTGTCCCGAGAGATCTGGCTGACTTCCAGAGTACCTGAGCAAG 289
 |||||||
 QY 661 accagaaataactcaaccactcgaatacaacagagagctccacagtaagaagctgctcg 720
 |||||||
 Db 288 ACCAGCAATGACTCTACCGACTCTGGAATACACAGAGGCTCCACAGGTAAAGAGCTGCTG 229

QY 721 atgaagctgtgtgtaaccttaagagcagagatcaatgctcgtcattctgtccactgctcag 780
 |||||||
 Db 228 ATGAAGCTGTGTGTAACCTTAAGAGCAGAGATCAATGCTGTGCTGCTGCTGCTGCTG 169
 |||||||
 QY 781 atcgaaggactctgtgcaatctcagccctgtgttaatgtaacagtgcaagatgact 840
 |||||||
 Db 168 ATCGACAGGACTCTGGCAATCCTCAGCCCTGTGTAATGCTCCAGTGCACAGTACTAT 109
 |||||||
 QY 841 taccgagccacagcgctctgtcacatcgcacattgaaagaagaggtctgcaagtgtgag 900
 |||||||
 Db 108 TACCGAGGCCACAGCGCTGTGCACATCGCCATTGAAAGAGGAGTGTGAGTGTGAAG 49
 |||||||
 QY 901 ctctctgtgagaatggggccaatgtgcatgccccgagctgcgagcgc 948
 |||||||
 Db 48 CTCCTGTGTGAGAAATGGGGCAATGTGCTATGCCGGGCTCGCGCGC 1

RESULT 10
 BF690154/c
 LOCUS 602186482r1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298445 3', DEFINITION
 mRNA sequence.
 ACCESSION BF690154
 VERSION BF690154.1 GI:11975562
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 984)
 NIH-MGC <http://mhc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC/DC/D/DP
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L1CM1154 row: c column: 22
 High quality sequence start: 20
 High quality sequence stop: 715.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4298445"
 /clone_1ib="NIH_MGC_49"
 /tissue_type="melanotic melanoma, high MDR (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAG(G). Size-selected using >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

BASE COUNT 200 a 297 c 284 g 203 t
 ORIGIN

Query Match 19.7%; Score 554; DB 168; Length 984;
 Best Local Similarity 86.6%; Pred. No. 2.7e-115;
 Matches 752; Conservative 0; Mismatches 95; Indels 21; Gaps 12;

QY 1870 gtgctggtctggtcgaactcttaactatacagtggtctccagcacagagcatctac 1929
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Db	893	GTGCTTGGCTGCGTGCACA -CTTCTTAACTAACACCCCTTGGCTCCAGACACTACAGACATTGAC	835
Oy	1930	agtcataatgatccagaagtgatcatccctgcggagacctgtctgtccctctgtacttaactta	1989
Db	834	ACTGTCAAGATCCAGAAATCAATCCCGCGGGAACCTGTGCCGTCCATGCTCATGTACTAG	775
Oy	1990	gtcttccttcttcggtctgtcgttag ---cccttgtagcctcttagccagtaggtcttgcg	2045
Db	774	TCTTCTCTTTTCGGGCTTCGACTGTGTACCCCTGTGGAGCTGTGGACCGACGGAGGCTTTGG	715
Oy	2046	ccccgaag -----ctctacagagccccaatgac--acagatcagtgtagcccatgga -g	2097
Db	714	CGCCACGACAAGCTCCCGCTACAGAGGCCCCAAATGCCAACAAGATCATAGTACGCCCATG	655
Oy	2098	ggacagagagagcagagggcaacgcygggcccagtagacaggggtatcctctgaaacccctctgag	2157
Db	654	GGACAGCGAAGACGAGAGGCAACGGGGCCCAAGTACAGAGGGTATCTCGAAGACCTCTTGGAG	595
Oy	2158	ctctc -tcaaatcaaccatcaggtcattggg -cagagcttggccctcccaagagagagtgtaacttc	2215
Db	594	CTCTCTCAAGCTACCAATCGGAGCTATGGGTCGAGCTGGCCCTTCAGAGAGACGTGACCTTCC	535
Oy	2216	gcgcagatagtcgtcgtctgtctg -ctgcctgcccacgtgtcctcctcaactaatctctctc	2274
Db	534	GCGGATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	475
Oy	2275	aacatgctcatcgcgcctcatatgagcagagacgclcaacagtgctgcacactgacagcttgagc	2334
Db	474	AACATGCTCATTCGCGCCCTCATGAGCGAGACCGTCAACAAGTGTCCGACATGACAGCTGGAGC	415
Oy	2335	a -tctggaaagctgcagaaagccatctctctcttgagatgtagaagtgtctatgtgtgtg	2393
Db	414	ATTCTGGAAGCTGCAGAAAGCCATCTGTCTGTGAGATGGAGAATGGCTATTGTGTGTG	355
Oy	2394	cagagagaag--caagcggcaggtgtgta -ctgacgcttgcaactaagccagatgtgcag	2450
Db	354	CAGGAAGAAGTACAGGGGACAGGTGTATGTACTGACCTTGCTGAACATGAGCTGAGTGGCAG	295
Oy	2451	cccggaatgacgctgtgtgtctcaagggtgagagaggtgtaacttgggcttcatatgtagacagac	2510
Db	294	CCCCGATGAGGGCTGTGCTTCAAGGCTGGAGAGGTGAATCTGGGCTTCATGTGGAGCAGAC	235
Oy	2511	gtctcctaagctgtgtgtgagaccgctcagggcaggtgtctccctggaactctgcag -aac	2569
Db	234	GCTGCTCACTGCTGTGTGAGGACCCCTCAGGGGACAGGTGTCCCTCGAAGCTTCGAGAAACC	175
Oy	2570	ctgtctctgtgtctccctcccaagagagatgtagatgtgtcctcttgagaaacatctgtgc	2629
Db	174	CTGTCTCTGGCTTCCCTCCCAAGAGGATGTAGATGTGTCTGTGAGGAAAAACATATGTGC	115
Oy	2630	ccgtccagctcctctccagtcacactgatatgcccagatgcagcagagagcagagagacagag	2689
Db	114	CCGTCCACTCTCTCCAGTCCAACTGATGTGGCCCAAGTGCAGACGAGAGGCCAGAGGGACAGA	55
Oy	2690	cagaggaatcttccaaccacatctgtct 2717	
Db	54	GCAGAGATCATTTCCAACCACTATGTGCTG 27	
RESULT 11			
LOCUS	BF433303/c		
DEFINITION	7606f10.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3702691 3		
ACCESSION	BF433303		
VERSION	BF433303.1		
KEYWORDS	EST		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 543)		

AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap/ .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbsr@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmerich-Buck, M.D., Ph.D.
	CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN, send email to: info@image.lnl.nl
FEATURES	Seq primer: -400P from Glibco High quality sequence stop: 399.
SOURCE	Location/Qualifiers 1..543 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:3702691" /clone_1lb="NCI-CGAP-Lu24" /tissue_type="carcinoid" /lab_host="DH10B" /note="Organ: lung; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker. Plasmid DNA from the normalized library NCI-CGAP-Lu5 was prepared, and ss circles were made in vitro. Following Hsp purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 141920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT	116 a 164 c 148 g 115 t .
ORIGIN	
Query Match	19.1%; Score 536.6; DB 148; Length 543;
Best Local Similarity	99.3%; Pred. No. 2.1e-111;
Matches 539; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
Dn 2227	ctgctcgtctgtcgtgcacgtgctgtgtcaactatcatctgtctgtcctaagaagtccatc 2286
Dn 543	CTGCTGTGTTGGTGCTGCCTACGTGCTGTCATCATCTGCTCACAATGCTCAATC 484
Oy 2287	gccctcatgaagcagaaaccgltcaaacagtgttcggacctgacaagcttgagaactgtga 2346
Dn 483	GCCCTCATGAAGCAGAACCCTGTAACAGTGTGCGCACTGACACTGGAGCATCTGGAAAGCTG 424
Oy 2347	cagaaaggcaatctgtctctgagaaatgagaatgtctattgttgtgtagagaagaagcag 2406
Dn 423	CAGAAAGCCAATCTGTCTCTGAGATGAGAAATGGCTATTGGTGTGCAAGCAAGAACG 364
Oy 2407	cgggcaggtgatgatctgacacgtttlgacactaaagcagaaatgagaccggatgatgcgttgg 2466
Dn 363	CGGGCAGGTGATGATCTCAACGTTGGCACTAAGCAAGATMGAGAGCGCGGATGAGGCTGG 304
Oy 2467	tgtctcaggttgtagaagaagtgaactgggtctccaatgagaagcagaagcgctgcttaagctgtgt 2526
Dn 303	TGCTTCAAGGTGTCAGAGAGGTGAACAGTGCGCTTCATGAGAGCACAGACCTCCTCAACGCTGTGT 244
Oy 2527	gagagaccgttcagagggagaggtgtccctctgaaactccgaagaacctgtctctgagcttcgct 2586
Dn 243	GAGGACCCGTCAGAGGGGACAGGTGTCCCTCTGAACTCTCGAAGAACCTGTCTCTGCTTCCCCT 184
Oy 2587	cccagaagaggaatgaagatgtgtgctctctgagaanaaactatgtgcccgtccagctccacag 2646
Dn 183	CCCAAAGGAGATGTAGAGATGTGCTCTCTGAGGAAAACATGTGTGCCGTCCACTCTCTCCAG 124
Oy 2647	tccaactgatgtccccagatgtcagaagaaggccagaaggaagaagaagaatctttccaac 2706
Dn 123	TCCAACGTATGAGCCAGATGTGACGAGGAGGCGCAGAGGACAGATCCAGAGATCTTTCCAC 64

QY	2707	caacatctctgctctggggtccagtgtaattctggtgcaatatattcttcacac	2766
Db	63	CACATCTCTGCTCTGGGCTGTGGGTCCTCCAGTAATTCGTGTGGCAATATATATTTTCTACTGAC	4
QY	2767	tca 2769	
Db	3	tca 1	
RESULT 12			
LOCUS	BF195711		
DEFINITION	BF195711	550 bp mRNA	EST 03-NOV-2000
ACCESSION	7n7r7e08.x1	NCI-CGAP Ov18 Homo sapiens CDNA IMAGE:3571671	3'
VERSION	Similar to TF:G9Y670	G9Y670 VANILLOID RECEPTOR-LIKE PROTEIN.	;
KEYWORDS	RNA sequence.		
SOURCE	BF195711		
ORGANISM	BF195711.1	GI:11082865	
REFERENCE	EST.		
AUTHORS	human.		
TITLE	Homo sapiens		
JOURNAL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
COMMENT	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 550)		
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .		
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-r@mail.nih.gov		
	Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael		
	R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento		
	Soares, Ph.D. CDNA Library Arrayed by: Christina Prange, The		
	I.M.A.G.E. Consortium DNA Sequencing by: Washington University		
	Genome Sequencing Center		
	Clone distribution: NCI-CGAP clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LINL, send email to:		
	info@image.lnll.gov		
	Trace considered overall poor quality		
	High quality sequence stop: 1.		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:3571671"		
	/clone_lib="NCI-CGAP Ov18"		
	/tissue_type="fibrotheoma"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: ovary; Vector: pTR7D-Pac (Pharmacia) with a		
	modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st		
	strand CDNA was primed with a GACATTTTCTTTTCTTTTCTTTT 3';		
	TGTTACCACTGTAAGTGGGCGCGCGGAGACATTTTCTTTTCTTTTCTTTT 3';		
	double-stranded CDNA was ligated to Eco RI adaptors		
	(Pharmacia), digested with Not I and cloned into the Not		
	I and Eco RI sites of the modified pTR73 vector. Library		
	went through one round of normalization, and was		
	constructed by Bento Soares and M. Fatima Bonaldo.		
	"		
BASE COUNT	122 a 166 c 149 g 113 t		
ORIGIN			
Query Match	19.0%, Score 532.4; DB 145; Length 550;		
Best Local Similarity	98.0%; Pred. No. 1.9e-110;		
Matches 539; Conservative 0; Mismatches 11; Indels 0; Gaps 0;			
QY	984	cggtagagctacccctctttgtgcccgtgtgacccaagcagcgggagatgtgtaagctact	1043
Db	1	CGGTAGCTACCCCTCTCTTGTGGCGCTTTGGACCAAGCAGTGGCATGTGTAGCTACT	60
QY	1044	ctgtgaagaccacacacacacgcgcgcagcgtcgaagccactgaactccacagggcaacacgt	1103
Db	61	CCTGAGAACCCACACACGACGCCGCCAGCTGACAGGCCACTGACTCCAGGCGCAACACAGA	120
QY	1104	ctgtcagctcctagtgtgatcatctcgagacaactcagcgtgagacaattgactcgtgtgaccag	1163

[illegible]

ORIGIN

Query Match 18.6%; Score 522.8; DB 117; Length 527;
Best Local Similarity 99.4%; Pred. No. 2.8e-108;
Matches 524; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 399 gacattgatgagagcagaagaatgctctgaggcgagacagagaagctgtgatttg 458
|||||
DB 527 GACATTGATGAGAGCCAGAGAGATGCTCGAGCGGACAGAGAAAGCTGATTTTGG 468
QY 459 gaggggctcctccctcctgtagtccaggtccagggcgagaccggaattccgctca 518
|||||
DB 467 GAGGGGCTCCTCCCTCCATGAGTACAGTTCAGGGGAGAGCCGAGATTTCGCCCTCA 408
QY 519 gataagatcaactcaactcaccgaaggagagagtgccagtcagccgagatccaaacg 578
|||||
DB 407 GATAAGAGTCAACTCAACTCACTCAAGAGAGAGAGAGTCCAGTCAAGCCGATCCAAACG 348
QY 579 attgaccgagatcgctctcctcaatgcggtctccgggggtgtcccgagagatctgtg 638
|||||
DB 347 ATTGACCGAGATGCGCTCTTCATGCGGTCTCCCGGGGTCTCCCGAGATCTGGCTGG 288
QY 639 acttccagatgactgagcagaagcagaagtaactcaaccgactcggaatacacagagg 698
|||||
DB 287 ACTTCCAGAGTACCTGAGCAAGACCAACCACTACCCAGCTCGGATACACAGAGGG 228
QY 699 ctccacagtgaaagacgtgctgtagaaggtgtgtgaaccttaagagcagagtcagtgc 758
|||||
DB 227 CTCACACAGTAAAGACGTGCTGATGAAAGGCTGTCTGTAACCTTAAAGAGGGGTCATATC 168
QY 759 ctgcatctgacctgctgtagatcgacagagagactctggaatccctcagccctgtgtaa 818
|||||
DB 167 CTGATCTGCTGCACTGCTGCGATGCGACCGGAGCTTGCGCAATCTCAGCCCTGGTAA 108
QY 819 tgcacatgacagatgactattacccagagccagacgctctgacatcgccattgagaa 878
|||||
DB 107 TGCCCAATGACAGATACATATACGAGAGGCGACGCTCTGCACATCGCATTTGAGAA 48
QY 879 gaagagctgcaagtgtgtgaagctcctgtgtgagaatgagggcaatg 925
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DB 47 GAGAGTCTGCACTGTGTGAAGCTCTGTGTGAGATGAGGAGCCCAATG 1

RESULT 14
BE670695/c
LOCUS BE670695 536 bp mRNA EST 08-SEP-2000
DEFINITION 738H05.x1 NCL:CGAP_Lu24 Homo sapiens CDNA clone IMAGE:3284793 3'
similar to TR:035433 035433 VANILLOID RECEPTOR SUBTYPE 1.; mRNA
sequence.
ACCESSION BE670695
VERSION BE670695
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 536)
NCL-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL, send email to:
infoimage.lnl.gov
Seq primer: -400P from Gibco

High quality sequence stop: 438.
Location/Qualifiers

FEATURES

source

1..536

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/db_xref="taxon:9606"

/clone="IMAGE:3284793"

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/lab_host="DH10B"

/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCL-CCGAP_Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonids
141920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT

111 a 161 c 143 g 121 t

ORIGIN

Query Match 18.6%; Score 522.2; DB 138; Length 536;
Best Local Similarity 98.5%; Pred. No. 3.9e-108;
Matches 527; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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DB 535 TGCTGGCATAGCTGCTCTGTCATACATCCGACTGCTCAACATGCTCATGCCCTCATGA 476
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QY 2357 tctctgctcctggaatgagagatgctatttggtgtgcaggaagaagcagggcagtg 2416
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DB 415 TCTATGTCCTGAGATGAGATGAGATGCTATGCTGCTGAGGAAACACAGCGGCGACGTG 356
QY 2417 tgatgctgacgctgtgacactaagcagatggaacccggaagcagcgtgtgtcctcaggg 2476
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QY 2477 tggaggaagtgaactggtctcatgaggagcagacgctgctcagctgtgtgaggaacct 2536
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DB 235 CAGGGGAGGTGCTCCCTGCAACTCTGCAAGACCTGTCTGCTGCTCCCTCCCAAGAGG 176
QY 2597 atgagagatggtgctctggaagaaactatgtgccgctcagcctcctcagtcacagat 2656
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DB 175 ATGAGATGCTGCTCTGAGAGAAACTATGTGCCCTGCTCAGCTCTCCAGCTCAACTGAT 116
QY 2657 ggcacagatgacagcagagagcagagagacagagagagatcttccaacacatctgt 2716
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DB 115 GGCCCAATGACAGCAGAGAGGCGACAGAGAGAGAGAGATCTTCCAAACACATCTGCT 56
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DB 55 GGCCTGGGGTCCAGTGAATTCGTGTGGCAATATATATTTCACCTACTCAAA 1

RESULT 15
BF436096/c
LOCUS BF436096 513 bp mRNA EST 30-MAR-2001
DEFINITION nab77a02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:3273507 3' similar to TR:09Y5S1 09Y5S1 VANILLOID
RECEPTOR-LIKE PROTEIN 1.; contains Alu repetitive element.; mRNA
sequence.
ACCESSION BF436096
VERSION BF436096
KEYWORDS EST.
EST. 11448411

SOURCE human.

ORGANISM Homo sapiens

REFERENCE
1. Haces 1 to 513.
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi.
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 513)

TITLE National Cancer Institute, Cancer Genome Anatomy Project

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: strausberg@ucla.edu

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

Seq primer: -40UP from Gibco

High quality sequence stop: 423.

FEATURES	Location/Qualifiers
source	1. .513

Source

1.513

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3 modified polymer: site 1: Not I; Site 3: Eco RI;
/hole=Ufgah: vector: p1/13D-Pac (Pharmacia) with

Soares and M. Fatima Bonaldo."

ORIGIN

Query Match	Score	DB	Length
18.38;	513;	148;	513;

Best Local Similarity 100.0%; Pred. No. 4.8e-106;

Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	421	gatgctctctagagcgagacagagaaagcttgatttttggagcgggctgcctcccatlgag	480
Db	453	GATGCTCTGTAGGCGGAGACAGAGAAAGCTGGATTTTTGGAGGGGGCTGCTCCCATGAG	394
QY	481	tcacagttccagggcgagagaccggaattcgccccatagataagatgtaactcctaactac	540
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